

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/997,868A  
Source: 1FW16  
Date Processed by STIC: 4/20/05

# *ENTERED*



IFW16

## RAW SEQUENCE LISTING

DATE: 04/20/2005

PATENT APPLICATION: US/09/997,868A

TIME: 08:17:48

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\04202005\I997868A.raw

3 <110> APPLICANT: Gorman, Cornelia M.  
 4 Groskreutz, Debyra J.  
 6 <120> TITLE OF INVENTION: PROHORMONE CONVERTASE TRANSFORMED CELLS AND POLYPEPTIDE  
 SYNTHESIS

8 <130> FILE REFERENCE: 11669.103USW3  
 10 <140> CURRENT APPLICATION NUMBER: US 09/997,868A  
 11 <141> CURRENT FILING DATE: 2001-11-28  
 13 <150> PRIOR APPLICATION NUMBER: US 08/026,143  
 14 <151> PRIOR FILING DATE: 1993-03-01  
 16 <150> PRIOR APPLICATION NUMBER: PCT/US92/10621  
 17 <151> PRIOR FILING DATE: 1992-12-04  
 19 <150> PRIOR APPLICATION NUMBER: US 07/887,265  
 20 <151> PRIOR FILING DATE: 1992-05-22  
 22 <150> PRIOR APPLICATION NUMBER: US 07/803,631  
 23 <151> PRIOR FILING DATE: 1991-12-06  
 25 <160> NUMBER OF SEQ ID NOS: 61  
 27 <170> SOFTWARE: PatentIn version 3.3  
 29 <210> SEQ ID NO: 1  
 30 <211> LENGTH: 2355  
 31 <212> TYPE: DNA  
 32 <213> ORGANISM: Murine  
 34 <400> SEQUENCE: 1

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 37 gtgagaacaa ggttttgagc catggagcaa agaggttgga ctctgcagtg tactgctttc 120  
 39 gccttctttt gcgtttggtg tgcactaagc agtgtaaaag caaagaggca gtttgtaaat 180  
 41 gaatgggagg cggagatccc cggagggcaa gaagctgcct ctgccatcgc cgaagaactg 240  
 43 gggatgacc ttttggtgca gattggatca cttgaaaatc actatttatt caaacacaaa 300  
 45 agccatcctc ggaggtcccg aagaagcgct cttcatatca ctaagagggt atctgatgat 360  
 47 gatcgtgtga cgtgggctga acaacagtat gaaaaagaga gaagtaaagc ttcagttcaa 420  
 49 aaagactcag cattggatct cttcaatgat ccaatgtgga atcagcagtg gtacttgcaa 480  
 51 gataccagaa tgactgcagc tctgcccagg ctggaccttc atgtaatacc tgtttgggaa 540  
 53 aagggtatta ctggcaagg agttgttatt actgtactgg atgatggctt ggagtggaa 600  
 55 cacacagaca tttatgccaa ttatgatcca gaggctagct atgattttaa cgataatgat 660  
 57 catgatccat tccccgata tgatctcaca aatgaaaaca aacatggaac aagatgtgca 720  
 59 ggtgaaattg ccatgcaagc aaataatcac aagtgtgggg ttggagttgc atataattcc 780  
 61 aaagttggag gcataagaat gctggatggc attgtaactg atgccattga ggctagtcca 840  
 63 attggattca accctggcca tgtggatatt tacagtgcaa gctggggccc taatgatgat 900  
 65 ggaaaaactg tggagggggc tggcagacta gcccagaagg catttgaata tgggtgcaaa 960  
 67 caggggagac aagggaaagg ctccatcttt gtctgggctt cagggaatgg gggctgcag 1020  
 69 ggagataact gtgactgtga tggctacaca gacagcattt acaccatctc tatcagcagt 1080  
 71 gcctcccagc aaggcctgtc accttggtat gcagagaagt gttcttcac attggctacc 1140  
 73 tcctacagca gtggtgatta cacagaccag cgaataacaa gcgctgacct gcacaatgac 1200  
 75 tgcacagaga cccacacagg cacctcggct tcagcaccct tggctgctgg tatctttgct 1260  
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79 acctctgagt acgacccatt ggccagtaac ccaggttgga aaaagaatgg ggcaggcttg 1380
81 atggtgaaca gccgatttgg atttggttg ctaaagcca aagctctggt ggatttggct 1440
83 gatcctcgga cctggagaaa tgtgcctgag aagaaagaat gtgttgtaaa agacaataac 1500
85 tttgagccta gagccctgaa agctaattga gaagtaattg ttgaaatccc aacaagagct 1560
87 tgtgaaggac aagaaaatgc tatcaagtct ctggaacatg tgcaatttga agcaacaatt 1620
89 gaatattctc gttagaggaga cttcatgtc acactcactt ctgctgttg aaccagcact 1680
91 gtactgttg ctgaaagga aagagataca tcccccaatg gctttaagaa ttgggacttc 1740
93 atgtctgttc atacatgggg agagaatcct gtaggcacct ggacattgaa aattacagac 1800
95 atgtctggaa gaatgcaaaa tgaaggaagg attgtgaact ggaagttgat tttgcatggg 1860
97 acatcttctc aaccagagca catgaagcag ccccggtgtg acacatccta caatacagtc 1920
99 cagaatgaca ggagaggagt ggaaaagatg gtgaatgttg tggagaagcg gccacacaa 1980
101 aagagcctga atggcaatct cctggtaccc aaaaactcca gcagcagcaa tgtggagggt 2040
103 agaagggatg agcaggtaca aggaactcct tcaaaggcca tgctgcgact cctacaaagt 2100
105 gcttttagca agaatgcact ttcaaaacaa tcaccaaaga agtctccaag tgcaaagctc 2160
107 agcatccctt atgaaagttt ctatgaagcc ttggaaaagc ttaacaagcc ctccaagctt 2220
109 gaaggctctg aagacagtct gtacagtgc tatgttgatg tattctataa cacaaaacct 2280
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113 taaaataagg agctc 2355
116 <210> SEQ ID NO: 2
117 <211> LENGTH: 2012
118 <212> TYPE: DNA
119 <213> ORGANISM: Murine
121 <400> SEQUENCE: 2
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124 cttttcactc ccaaagaagg atggagggcg gttgtggatc ccagtggaag gcggccgggt 120
126 tcctcttctg tgtgatggtt tttgcgtctg ccgagagacc cgtcttcacg aatcattttc 180
128 ttgtggagtt gcataaagac ggagaggaag aggctcgcca agttgcagca gaacacggct 240
130 ttggagtcgg aaagctcccc tttgcagaag gcctgtatca cttttatcac aatgggcttg 300
132 caaaggccaa aagaagacgc agcctacacc ataagcggca gctagagaga gaccccagga 360
134 taaagatggc gctgcaacaa gaaggatttg accgtaaaaa gagagggtac agggacatca 420
136 atgagattga catcaacatg aatgatcctc tctttacaaa gcaatggtac ctgttcaaca 480
138 ctgggcaagc cgatggaact cctgggctag acttgaacgt ggccgaagcc tgggagctgg 540
140 gatacacagg aaaaggagtg accattggaa ttatggatga tggaaattgac tatctccacc 600
142 cagacctggc ctacaactac aacgctgatg caagtattga cttcagcagc aatgaccctt 660
144 acccataccc tcgatacaca gatgactggt tcaacagcca tggaaactagg tgtgcaggag 720
146 aagttttctg tcgagccagc aacaatatct gtggagtctg cgtagcatac aactccaagg 780
148 tggcagggat ccgatgctg gaccagccct ttatgacaga catcatcgaa gcctcctcca 840
150 tcagccacat gcctcaactg atcgacatct acagtgaag ctggggcccc acagacaatg 900
152 ggaagacggt tgatgggccc cgagagctca cactccaggc catggctgat ggcgtgaaca 960
154 agggccgtgg gggcaaaagg agcatctatg tgtgggcctc tggggacggt ggcagctacg 1020
156 atgactgcaa ctgtgacggc tatgcttcaa gcatgtggac catctccatc aactcagcca 1080
158 tcaatgatgg caggactgcc ttgtatgatg agagtgtctc ttccacctta gcatccacct 1140
160 tcagcaatgg gaggaagagg aatcctgagg ctggtgtggc taccacagac ttgtatggca 1200
162 actgtactct gagacactct gggacatctg cagctgctcc ggaggcagct ggcgtgtttg 1260
164 cattagcttt ggaggctaac ctggatctga cctggagaga catgcaacat ctgactgtgc 1320
166 tcacctcaa gcggaaccag cttcatgatg aggttcatca gtggcgacgg aatgggggtg 1380
168 gcctggaatt taatcacctc tttggctacg gagtccttga tgcagggtgc atggtgaaaa 1440
170 tggctaaaga ctggaaaact gttccggaga gattccattg tgtgggaggc tctgtgcaga 1500
172 accctgaaaa aataccaccc accggcaagc tggtagtgac cctcaaaaca aatgcatgtg 1560

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174 aggggaagga aaacttcgtc cgctacctgg agcacgtcca agctgtcatc acagtcaacg 1620
176 cgaccaggag aggagacctg aacatcaaca tgacctcccc aatgggcacc aagtcattt 1680
178 tgctgagccg gcgtcccaga gacgacgact ccaaggtggg ctttgacaag tggcctttca 1740
180 tgaccaccca cacctggggg gaggtgccc gagggacctg gacctggag ctgggggttg 1800
182 tgggcagtgc accacagaag gggttgctga aggaatggac cctgatgctt cacggcacac 1860
184 agagcgcccc atacatcgat caggtggtga gggattacca gtctaagctg gccatgtcca 1920
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192 <211> LENGTH: 753
193 <212> TYPE: PRT
194 <213> ORGANISM: Murine
196 <400> SEQUENCE: 3
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199 1 5 10 15
202 Cys Val Trp Cys Ala Leu Ser Ser Val Lys Ala Lys Arg Gln Phe Val
203 20 25 30
206 Asn Glu Trp Ala Ala Glu Ile Pro Gly Gly Gln Glu Ala Ala Ser Ala
207 35 40 45
210 Ile Ala Glu Glu Leu Gly Tyr Asp Leu Leu Gly Gln Ile Gly Ser Leu
211 50 55 60
214 Glu Asn His Tyr Leu Phe Lys His Lys Ser His Pro Arg Arg Ser Arg
215 65 70 75 80
218 Arg Ser Ala Leu His Ile Thr Lys Arg Leu Ser Asp Asp Asp Arg Val
219 85 90 95
222 Thr Trp Ala Glu Gln Gln Tyr Glu Lys Glu Arg Ser Lys Arg Ser Val
223 100 105 110
226 Gln Lys Asp Ser Ala Leu Asp Leu Phe Asn Asp Pro Met Trp Asn Gln
227 115 120 125
230 Gln Trp Tyr Leu Gln Asp Thr Arg Met Thr Ala Ala Leu Pro Lys Leu
231 130 135 140
234 Asp Leu His Val Ile Pro Val Trp Glu Lys Gly Ile Thr Gly Lys Gly
235 145 150 155 160
238 Val Val Ile Thr Val Leu Asp Asp Gly Leu Glu Trp Asn His Thr Asp
239 165 170 175
242 Ile Tyr Ala Asn Tyr Asp Pro Glu Ala Ser Tyr Asp Phe Asn Asp Asn
243 180 185 190
246 Asp His Asp Pro Phe Pro Arg Tyr Asp Leu Thr Asn Glu Asn Lys His
247 195 200 205
250 Gly Thr Arg Cys Ala Gly Glu Ile Ala Met Gln Ala Asn Asn His Lys
251 210 215 220
254 Cys Gly Val Gly Val Ala Tyr Asn Ser Lys Val Gly Gly Ile Arg Met
255 225 230 235 240
258 Leu Asp Gly Ile Val Thr Asp Ala Ile Glu Ala Ser Ser Ile Gly Phe
259 245 250 255
262 Asn Pro Gly His Val Asp Ile Tyr Ser Ala Ser Trp Gly Pro Asn Asp
263 260 265 270
266 Asp Gly Lys Thr Val Glu Gly Pro Gly Arg Leu Ala Gln Lys Ala Phe
267 275 280 285

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270 Glu Tyr Gly Val Lys Gln Gly Arg Gln Gly Lys Gly Ser Ile Phe Val
271      290      295      300
274 Trp Ala Ser Gly Asn Gly Gly Arg Gln Gly Asp Asn Cys Asp Cys Asp
275 305      310      315      320
278 Gly Tyr Thr Asp Ser Ile Tyr Thr Ile Ser Ile Ser Ser Ala Ser Gln
279      325      330      335
282 Gln Gly Leu Ser Pro Trp Tyr Ala Glu Lys Cys Ser Ser Thr Leu Ala
283      340      345      350
286 Thr Ser Tyr Ser Ser Gly Asp Tyr Thr Asp Gln Arg Ile Thr Ser Ala
287      355      360      365
290 Asp Leu His Asn Asp Cys Thr Glu Thr His Thr Gly Thr Ser Ala Ser
291      370      375      380
294 Ala Pro Leu Ala Ala Gly Ile Phe Ala Leu Ala Leu Glu Ala Asn Pro
295 385      390      395      400
298 Asn Leu Thr Trp Arg Asp Met Gln His Leu Val Val Trp Thr Ser Glu
299      405      410      415
302 Tyr Asp Pro Leu Ala Ser Asn Pro Gly Trp Lys Lys Asn Gly Ala Gly
303      420      425      430
306 Leu Met Val Asn Ser Arg Phe Gly Phe Gly Leu Leu Asn Ala Lys Ala
307      435      440      445
310 Leu Val Asp Leu Ala Asp Pro Arg Thr Trp Arg Asn Val Pro Glu Lys
311      450      455      460
314 Lys Glu Cys Val Val Lys Asp Asn Asn Phe Glu Pro Arg Ala Leu Lys
315 465      470      475      480
318 Ala Asn Gly Glu Val Ile Val Glu Ile Pro Thr Arg Ala Cys Glu Gly
319      485      490      495
322 Gln Glu Asn Ala Ile Lys Ser Leu Glu His Val Gln Phe Glu Ala Thr
323      500      505      510
326 Ile Glu Tyr Ser Arg Arg Gly Asp Leu His Val Thr Leu Thr Ser Ala
327      515      520      525
330 Val Gly Thr Ser Thr Val Leu Leu Ala Glu Arg Glu Arg Asp Thr Ser
331      530      535      540
334 Pro Asn Gly Phe Lys Asn Trp Asp Phe Met Ser Val His Thr Trp Gly
335 545      550      555      560
338 Glu Asn Pro Val Gly Thr Trp Thr Leu Lys Ile Thr Asp Met Ser Gly
339      565      570      575
342 Arg Met Gln Asn Glu Gly Arg Ile Val Asn Trp Lys Leu Ile Leu His
343      580      585      590
346 Gly Thr Ser Ser Gln Pro Glu His Met Lys Gln Pro Arg Val Tyr Thr
347      595      600      605
350 Ser Tyr Asn Thr Val Gln Asn Asp Arg Arg Gly Val Glu Lys Met Val
351      610      615      620
354 Asn Val Val Glu Lys Arg Pro Thr Gln Lys Ser Leu Asn Gly Asn Leu
355 625      630      635      640
358 Leu Val Pro Lys Asn Ser Ser Ser Ser Asn Val Glu Gly Arg Arg Asp
359      645      650      655
362 Glu Gln Val Gln Gly Thr Pro Ser Lys Ala Met Leu Arg Leu Leu Gln
363      660      665      670
366 Ser Ala Phe Ser Lys Asn Ala Leu Ser Lys Gln Ser Pro Lys Lys Ser

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367          675          680          685
370 Pro Ser Ala Lys Leu Ser Ile Pro Tyr Glu Ser Phe Tyr Glu Ala Leu
371          690          695          700
374 Glu Lys Leu Asn Lys Pro Ser Lys Leu Glu Gly Ser Glu Asp Ser Leu
375 705          710          715          720
378 Tyr Ser Asp Tyr Val Asp Val Phe Tyr Asn Thr Lys Pro Tyr Lys His
379          725          730          735
382 Arg Asp Asp Arg Leu Leu Gln Ala Leu Met Asp Ile Leu Asn Glu Glu
383          740          745          750
386 Asn
390 <210> SEQ ID NO: 4
391 <211> LENGTH: 637
392 <212> TYPE: PRT
393 <213> ORGANISM: Murine
395 <400> SEQUENCE: 4
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398 1          5          10          15
401 Cys Val Met Val Phe Ala Ser Ala Glu Arg Pro Val Phe Thr Asn His
402          20          25          30
405 Phe Leu Val Glu Leu His Lys Asp Gly Glu Glu Glu Ala Arg Gln Val
406          35          40          45
409 Ala Ala Glu His Gly Phe Gly Val Arg Lys Leu Pro Phe Ala Glu Gly
410          50          55          60
413 Leu Tyr His Phe Tyr His Asn Gly Leu Ala Lys Ala Lys Arg Arg Arg
414 65          70          75          80
417 Ser Leu His His Lys Arg Gln Leu Glu Arg Asp Pro Arg Ile Lys Met
418          85          90          95
421 Ala Leu Gln Gln Glu Gly Phe Asp Arg Lys Lys Arg Gly Tyr Arg Asp
422          100          105          110
425 Ile Asn Glu Ile Asp Ile Asn Met Asn Asp Pro Leu Phe Thr Lys Gln
426          115          120          125
429 Trp Tyr Leu Phe Asn Thr Gly Gln Ala Asp Gly Thr Pro Gly Leu Asp
430          130          135          140
433 Leu Asn Val Ala Glu Ala Trp Glu Leu Gly Tyr Thr Gly Lys Gly Val
434 145          150          155          160
437 Thr Ile Gly Ile Met Asp Asp Gly Ile Asp Tyr Leu His Pro Asp Leu
438          165          170          175
441 Ala Tyr Asn Tyr Asn Ala Asp Ala Ser Tyr Asp Phe Ser Ser Asn Asp
442          180          185          190
445 Pro Tyr Pro Tyr Pro Arg Tyr Thr Asp Asp Trp Phe Asn Ser His Gly
446          195          200          205
449 Thr Arg Cys Ala Gly Glu Val Ser Ala Ala Ala Ser Asn Asn Ile Cys
450          210          215          220
453 Gly Val Gly Val Ala Tyr Asn Ser Lys Val Ala Gly Ile Arg Met Leu
454 225          230          235          240
457 Asp Gln Pro Phe Met Thr Asp Ile Ile Glu Ala Ser Ser Ile Ser His
458          245          250          255
461 Met Pro Gln Leu Ile Asp Ile Tyr Ser Ala Ser Trp Gly Pro Thr Asp
462          260          265          270

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 17,23,32  
Seq#:6; N Pos. 13,25,28  
Seq#:47; Xaa Pos. 1,2,3

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30  
Seq#:31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54  
Seq#:55,56,57,58

**VERIFICATION SUMMARY**

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L:582 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
L:1119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0